Sequence Listing

<110> DAVID P. DAVIS
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<120> COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
      TREATMENT OF TUMOR

<130> P1981R1P1-US

<140> US 10/656,598
<141> 2003-09-05

<150> US 60/410,166
<151> 2002-09-11

<160> 52

<210> 1
<211> 2470
<212> DNA
<213> Homo sapien

<400> 1
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aataaacttg caagaggact atgaaagatt atgatgaact tctcaaatat 200

tatgaattac atgaaactat tgggacaggt ggctttgcaa aggtcaaact 250

tgcctgccat atccttactg gagagatggt agctataaaa atcatggata 300

aaaacacact agggagtgat ttgccccgga tcaaaacgga gattgaggcc 350

ttgaagaacc tgagacatca gcatatatgt caactctacc atgtgctaga 400

gacagccaac aaaatattca tggttcttga gtactgccct ggaggagagc 450

tgtttgacta tataatttcc caggatcgcc tgtcagaaga ggagacccgg 500

gttgtcttcc gtcagatagt atctgctgtt gcttatgtgc acagccaggg 550

ctatgctcac agggacctca gccagaaaa tttgctgttt gatgaatatc 600

ataaattaaa gctgattgac tttggtctct gtgcaaaacc caagggtaac 650

aaggattacc atctacagac atgctgtggg agtctggctt atgcagcacc 700

1

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tgagttaata caaggcaaat catatcttgg atcagaggca gatgtttgga 750

gcatgggcat actgttatat gttcttatgt gtggatttct accatttgat 800

gatgataatg taatggcttt atacaagaag attatgagag gaaaatatga 850

tgttcccaag tggctctctc ccagtagcat tctgcttctt caacaaatgc 900

tgcaggtgga cccaaagaaa cggatttcta tgaaaaatct attgaaccat 950

ccctggatca tgcaagatta caactatcct gttgagtggc aaagcaagaa 1000

tccttttatt cacctcgatg atgattgcgt aacagaactt tctgtacatc 1050

acagaaacaa caggcaaaca atggaggatt taatttcact gtggcagtat 1100

gatcacctca cggctaccta tcttctgctt ctagccaaga aggctcgggg 1150

aaaaccagtt cgtttaaggc tttcttcttt ctcctgtgga caagccagtg 1200

ctaccccatt cacagacatc aagtcaaata attggagtct ggaagatgtg 1250

accgcaagtg ataaaaatta tgtggcggga ttaatagact atgattggtg 1300

tgaagatgat ttatcaacag gtgctgctac tccccgaaca tcacagttta 1350

ccaagtactg gacagaatca aatggggtgg aatctaaatc attaactcca 1400

gccttatgca gaacacctgc aaataaatta aagaacaaag aaaatgtata 1450

tactcctaag tctgctgtaa agaatgaaga gtactttatg tttcctgagc 1500

caaagactcc agttaataag aaccagcata agagagaaat actcactacg 1550

ccaaatcgtt acactacacc ctcaaaagct agaaaccagt gcctgaaaga 1600

aactccaatt aaaataccag taaattcaac aggaacagac aagttaatga 1650

caggtgtcat tagccctgag aggcggtgcc gctcagtgga attggatctc 1700

aaccaagcac atatggagga gactccaaaa agaaagggag ccaaagtgtt 1750

tgggagcctt gaaagggggt tggataaggt tatcactgtg ctcaccagga 1800

gcaaaaggaa gggttctgcc agagacgggc ccagaagact aaagcttcac 1850

tataatgtga ctacaactag attagtgaat ccagatcaac tgttgaatga 1900

aataatgtct attcttccaa gaagcatgt tgactttgta caaaagggtt 1950

atacactgaa gtgtcaaaca cagtcagatt ttgggaaagt gacaatgcaa 2000

tttgaattag aagtgtgcca gcttcaaaaa cccgatgtgg tgggtatcag 2050

gaggcagcgg cttaagggcg atgcctgggt ttacaaaaga ttagtggaag 2100

acatcctatc tagctgcaag gtataattga tggattcttc catcctgccg 2150
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2

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gatgagtgtg ggtgtgatac agcctacata aagactgtta tgatcgcttt 2200

gattttaaag ttcattggaa ctaccaactt gtttctaaag agctatctta 2250

agaccaatat ctctttgttt ttaaacaaaa gatattattt tgtgtatgaa 2300

tctaaatcaa gcccatctgt cattatgtta ctgtcttttt taatcatgtg 2350

gttttgtata ttaataattg ttgactttct tagattcact tccatatgtg 2400

aatgtaagct cttaactatg tctctttgta atgtgtaatt tctttctgaa 2450

ataaaaccat ttgtgaatat 2470
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<210> 2
<211> 651
<212> PRT
<213> Homo sapien

<400> 2

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Met Lys Asp Tyr Asp Glu Leu Leu Lys Tyr Tyr Glu Leu His Glu
  1               5                  10                  15

Thr Ile Gly Thr Gly Gly Phe Ala Lys Val Lys Leu Ala Cys His
                 20                  25                  30

Ile Leu Thr Gly Glu Met Val Ala Ile Lys Ile Met Asp Lys Asn
                 35                  40                  45

Thr Leu Gly Ser Asp Leu Pro Arg Ile Lys Thr Glu Ile Glu Ala
                 50                  55                  60

Leu Lys Asn Leu Arg His Gln His Ile Cys Gln Leu Tyr His Val
                 65                  70                  75

Leu Glu Thr Ala Asn Lys Ile Phe Met Val Leu Glu Tyr Cys Pro
                 80                  85                  90

Gly Gly Glu Leu Phe Asp Tyr Ile Ile Ser Gln Asp Arg Leu Ser
                 95                 100                 105

Glu Glu Glu Thr Arg Val Val Phe Arg Gln Ile Val Ser Ala Val
                110                 115                 120

Ala Tyr Val His Ser Gln Gly Tyr Ala His Arg Asp Leu Lys Pro
                125                 130                 135

Glu Asn Leu Leu Phe Asp Glu Tyr His Lys Leu Lys Leu Ile Asp
                140                 145                 150

Phe Gly Leu Cys Ala Lys Pro Lys Gly Asn Lys Asp Tyr His Leu
                155                 160                 165

Gln Thr Cys Cys Gly Ser Leu Ala Tyr Ala Ala Pro Glu Leu Ile
                170                 175                 180

Gln Gly Lys Ser Tyr Leu Gly Ser Glu Ala Asp Val Trp Ser Met
                185                 190                 195
```

3

```
Gly Ile Leu Leu Tyr Val Leu Met Cys Gly Phe Leu Pro Phe Asp
              200                 205                 210

Asp Asp Asn Val Met Ala Leu Tyr Lys Lys Ile Met Arg Gly Lys
              215                 220                 225

Tyr Asp Val Pro Lys Trp Leu Ser Pro Ser Ser Ile Leu Leu Leu
              230                 235                 240

Gln Gln Met Leu Gln Val Asp Pro Lys Lys Arg Ile Ser Met Lys
              245                 250                 255

Asn Leu Leu Asn His Pro Trp Ile Met Gln Asp Tyr Asn Tyr Pro
              260                 265                 270

Val Glu Trp Gln Ser Lys Asn Pro Phe Ile His Leu Asp Asp Asp
              275                 280                 285

Cys Val Thr Glu Leu Ser Val His His Arg Asn Asn Arg Gln Thr
              290                 295                 300

Met Glu Asp Leu Ile Ser Leu Trp Gln Tyr Asp His Leu Thr Ala
              305                 310                 315

Thr Tyr Leu Leu Leu Leu Ala Lys Lys Ala Arg Gly Lys Pro Val
              320                 325                 330

Arg Leu Arg Leu Ser Ser Phe Ser Cys Gly Gln Ala Ser Ala Thr
              335                 340                 345

Pro Phe Thr Asp Ile Lys Ser Asn Asn Trp Ser Leu Glu Asp Val
              350                 355                 360

Thr Ala Ser Asp Lys Asn Tyr Val Ala Gly Leu Ile Asp Tyr Asp
              365                 370                 375

Trp Cys Glu Asp Asp Leu Ser Thr Gly Ala Ala Thr Pro Arg Thr
              380                 385                 390

Ser Gln Phe Thr Lys Tyr Trp Thr Glu Ser Asn Gly Val Glu Ser
              395                 400                 405

Lys Ser Leu Thr Pro Ala Leu Cys Arg Thr Pro Ala Asn Lys Leu
              410                 415                 420

Lys Asn Lys Glu Asn Val Tyr Thr Pro Lys Ser Ala Val Lys Asn
              425                 430                 435

Glu Glu Tyr Phe Met Phe Pro Glu Pro Lys Thr Pro Val Asn Lys
              440                 445                 450

Asn Gln His Lys Arg Glu Ile Leu Thr Thr Pro Asn Arg Tyr Thr
              455                 460                 465

Thr Pro Ser Lys Ala Arg Asn Gln Cys Leu Lys Glu Thr Pro Ile
              470                 475                 480

Lys Ile Pro Val Asn Ser Thr Gly Thr Asp Lys Leu Met Thr Gly
```

4

```
Val Ile Ser Pro Glu Arg Arg Cys Arg Ser Val Glu Leu Asp Leu
                500                 505                 510

Asn Gln Ala His Met Glu Glu Thr Pro Lys Arg Lys Gly Ala Lys
                515                 520                 525

Val Phe Gly Ser Leu Glu Arg Gly Leu Asp Lys Val Ile Thr Val
                530                 535                 540

Leu Thr Arg Ser Lys Arg Lys Gly Ser Ala Arg Asp Gly Pro Arg
                545                 550                 555

Arg Leu Lys Leu His Tyr Asn Val Thr Thr Thr Arg Leu Val Asn
                560                 565                 570

Pro Asp Gln Leu Leu Asn Glu Ile Met Ser Ile Leu Pro Lys Lys
                575                 580                 585

His Val Asp Phe Val Gln Lys Gly Tyr Thr Leu Lys Cys Gln Thr
                590                 595                 600

Gln Ser Asp Phe Gly Lys Val Thr Met Gln Phe Glu Leu Glu Val
                605                 610                 615

Cys Gln Leu Gln Lys Pro Asp Val Val Gly Ile Arg Arg Gln Arg
                620                 625                 630

Leu Lys Gly Asp Ala Trp Val Tyr Lys Arg Leu Val Glu Asp Ile
                635                 640                 645

Leu Ser Ser Cys Lys Val
                650
```

<210> 3
<211> 2257
<212> DNA
<213> Homo sapien

<400> 3
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tgcatcaccc ggaccggggg attagctccg gtttgcatca cccggaccgg 100

gggccgggcg cgcacgagac tcgcagcgga agtggaggcg gctccgcgcg 150

cgtccgctgc taggacccgg gcagggctgg agctgggctg ggatcccgag 200

ctcggcagca gcgcagcggg ccggcccacc tgctggtgcc 'ctggaggctc 250

tgagccccgg cggcgcccgg gcccacgcgg aacgacgggg cgagatgcga 300

gccacccctc tagctgctcc tgcgggttcc ctgtccagga agaagcggtt 350

ggagttggat gacaacttag ataccgagcg tcccgtccag aaacgagctc 400

gaagtgggcc ccagcccaga ctgccccct gcctgttgcc cctgagccca 450
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cctactgctc cagatcgtgc aactgctgtg gccactgcct cccgtcttgg 500

gccctatgtc ctcctggagc ccgaggaggg cgggcgggcc taccaggccc 550

tgcactgccc tacaggcact gagtatacct gcaaggtgta ccccgtccag 600

gaagccccgg ccgtgctgga gccctatgcg cggctgcccc cgcacaagca 650

tgtggctcgg cccactgagg tcctggctgg tacccagctc ctctacgcct 700

ttttcactcg gacccatggg gacatgcaca gcctggtgcg aagccgccac 750

cgtatccctg agcctgaggc tgccgtgctc ttccgccaga tggccaccgc 800

cctggcgcac tgtcaccagc acggtctggt cctgcgtgat ctcaagctgt 850

gtcgctttgt cttcgctgac cgtgagagga agaagctggt gctggagaac 900

ctggaggact cctgcgtgct gactgggcca gatgattccc tgtgggacaa 950

gcacgcgtgc ccagcctacg tgggacctga gatactcagc tcacgggcct 1000

catactcggg caaggcagcc gatgtctgga gcctgggcgt ggcgctcttc 1050

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cttcggcaag atccgccgcg gggcctacgc cttgcctgca ggcctctcgg 1150

cccctgcccg ctgtctggtt cgctgcctcc ttcgtcggga gccagctgaa 1200

cggctcacag ccacaggcat cctcctgcac ccctggctgc gacaggaccc 1250

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tccctgatgg tctggggctg gacgaagcca gggaagagga gggagacaga 1350

gaagtggttc tgtatggcta ggaccaccct actacacgct cagctgccaa 1400

cagtggattg agtttggggg tagctccaag ccttctcctg cctctgaact 1450

gagccaaacc ttcagtgcct tccagaaggg agaaaggcag aagcctgtgt 1500

ggagtgtgct gtgtacacat ctgctttgtt ccacacacat gcagttcctg 1550

cttgggtgct tatcaggtgc caagccctgt tctcggtgct gggagtacag 1600

cagtgagcaa aggagacaat attccctgct cacagagatg acaaactggc 1650

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gggtacactt tgtaccagtg tcggcctcca ctgatgctgg tgctcaggca 1750

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cttgtacctt ttcagagaaa gggaggtatc cctgtgccaa aggctccagg 1850

cctctcccct gcaactcagg acccaagccc agctcactct gggaactgtg 1900
```

6

```
ttcccagcat ctctgtcctc ttgattaaga gattctcctt ccaggcctaa 1950

gcctgggatt tgggccagag ataagaatcc aaactatgag gctagttctt 2000

gtctaactca agactgttct ggaatgaggg tccaggcctg tcaaccatgg 2050

ggcttctgac ctgagcacca aggttgaggg acaggattag gcagggtctg 2100

tcctgtggcc acctggaaag tcccaggtgg gactcttctg gggacacttg 2150

gggtccacaa tcccaggtcc atactctagg ttttggatac catgagtatg 2200

tatgtttacc tgtgcctaat aaaggagaat tatgaaataa aaaaaaaaa 2250

aaaaaaa 2257
```

<210> 4
<211> 358
<212> PRT
<213> Homo sapien

<400> 4
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Met Arg Ala Thr Pro Leu Ala Ala Pro Ala Gly Ser Leu Ser Arg
 1               5                  10                  15

Lys Lys Arg Leu Glu Leu Asp Asp Asn Leu Asp Thr Glu Arg Pro
                20                  25                  30

Val Gln Lys Arg Ala Arg Ser Gly Pro Gln Pro Arg Leu Pro Pro
                35                  40                  45

Cys Leu Leu Pro Leu Ser Pro Pro Thr Ala Pro Asp Arg Ala Thr
                50                  55                  60

Ala Val Ala Thr Ala Ser Arg Leu Gly Pro Tyr Val Leu Leu Glu
                65                  70                  75

Pro Glu Glu Gly Gly Arg Ala Tyr Gln Ala Leu His Cys Pro Thr
                80                  85                  90

Gly Thr Glu Tyr Thr Cys Lys Val Tyr Pro Val Gln Glu Ala Pro
                95                  100                 105

Ala Val Leu Glu Pro Tyr Ala Arg Leu Pro Pro His Lys His Val
                110                 115                 120

Ala Arg Pro Thr Glu Val Leu Ala Gly Thr Gln Leu Leu Tyr Ala
                125                 130                 135

Phe Phe Thr Arg Thr His Gly Asp Met His Ser Leu Val Arg Ser
                140                 145                 150

Arg His Arg Ile Pro Glu Pro Glu Ala Ala Val Leu Phe Arg Gln
                155                 160                 165

Met Ala Thr Ala Leu Ala His Cys His Gln His Gly Leu Val Leu
                170                 175                 180
```

7

```
Arg Asp Leu Lys Leu Cys Arg Phe Val Phe Ala Asp Arg Glu Arg
              185             190             195

Lys Lys Leu Val Leu Glu Asn Leu Glu Asp Ser Cys Val Leu Thr
              200             205             210

Gly Pro Asp Asp Ser Leu Trp Asp Lys His Ala Cys Pro Ala Tyr
              215             220             225

Val Gly Pro Glu Ile Leu Ser Ser Arg Ala Ser Tyr Ser Gly Lys
              230             235             240

Ala Ala Asp Val Trp Ser Leu Gly Val Ala Leu Phe Thr Met Leu
              245             250             255

Ala Gly His Tyr Pro Phe Gln Asp Ser Glu Pro Val Leu Leu Phe
              260             265             270

Gly Lys Ile Arg Arg Gly Ala Tyr Ala Leu Pro Ala Gly Leu Ser
              275             280             285

Ala Pro Ala Arg Cys Leu Val Arg Cys Leu Leu Arg Arg Glu Pro
              290             295             300

Ala Glu Arg Leu Thr Ala Thr Gly Ile Leu Leu His Pro Trp Leu
              305             310             315

Arg Gln Asp Pro Met Pro Leu Ala Pro Thr Arg Ser His Leu Trp
              320             325             330

Glu Ala Ala Gln Val Val Pro Asp Gly Leu Gly Leu Asp Glu Ala
              335             340             345

Arg Glu Glu Glu Gly Asp Arg Glu Val Val Leu Tyr Gly
              350             355
```

<210> 5
<211> 1282
<212> DNA
<213> Homo sapien

<220>
<221> Unsure
<222> 898, 1187, 1198, 1241, 1262, 1266, 1277, 1281
<223> Unknown base

<400> 5
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 gggccactca aggacccagg acagagggaa gagggccaac ccagctggac 150

 cacaggcaaa ccccattgcc tttgagagaa agaagaggac ccggtgaaac 200

 atgctgctgc tgaagaaaca cacggaggac atcagcagcg tctacgagat 250

 ccgcgagagg ctcggctcgg gtgccttctc cgaggtggtg ctggcccagg 300
```

8

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agcggggctc cgcacacctc gtggccctca agtgcatccc caagaaggcc 350

ctccgggggca aggaggccct ggtggagaac gagatcgcag tgctccgtag 400

gatcagtcac cccaacatcg tcgctctgga ggatgtccac gagagccctt 450

cccacctcta cctggccatg gaactggtga cgggtggcga gctgtttgac 500

cgcatcatgg agcgcggctc ctacacagag aaggatgcca gccatctggt 550

gggtcaggtc cttggcgccg tctcctacct gcacagcctg gggatcgtgc 600

accgggacct caagcccgaa aacctcctgt atgccacgcc ctttgaggac 650

tcgaagatca tggtctctga ctttggactc tccaaaatcc aggctgggaa 700

catgctaggc accgcctgtg ggacccctgg atatgtggcc ccagagctct 750

tggagcagaa accctacggg aaggccgtag atgtgtgggc cctgggcgtc 800

atctcctaca tcctgctgtg tgggtacccc cccttctacg acgagagcga 850

ccctgagctc ttcagccaga tcctgagggc cagctatgag tttgactntc 900

ctttctggga tgacatctca gaatcaggca aagactttat tcggcacctt 950

ctggagcgag accttcagaa gaggttcacc tgccaacagg ccttgcggga 1000

cctttggatc ttttgggaca caggctttgg cagggacatc ttagggtttg 1050

tcagtgagca gatccggaag aactttgctt ggacacactg gaagcgagcc 1100

ttcaatgcca ccttgttcct gcgccacatc cggaagctgg ggcagatccc 1150

agagggcgag ggggcctctg agcagggcat ggsccgncac agccactnag 1200

gccttcgtgc tggccagccc cccaagtggt gatgcccagg nagatgccga 1250

ggccaagtgg antgancccc agatttnctt nc 1282
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<210> 6
<211> 343
<212> PRT
<213> Homo sapien

<220>
<221> Unsure
<222> 233, 328, 333
<223> Unknown amino acid

<400> 6
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 Met Leu Leu Leu Lys Lys His Thr Glu Asp Ile Ser Ser Val Tyr
   1               5                  10                  15

 Glu Ile Arg Glu Arg Leu Gly Ser Gly Ala Phe Ser Glu Val Val
                 20                  25                  30

 Leu Ala Gln Glu Arg Gly Ser Ala His Leu Val Ala Leu Lys Cys
```

```
                    35                      40                      45
Ile Pro Lys Lys Ala Leu Arg Gly Lys Glu Ala Leu Val Glu Asn
                    50                      55                      60

Glu Ile Ala Val Leu Arg Arg Ile Ser His Pro Asn Ile Val Ala
                    65                      70                      75

Leu Glu Asp Val His Glu Ser Pro Ser His Leu Tyr Leu Ala Met
                    80                      85                      90

Glu Leu Val Thr Gly Gly Glu Leu Phe Asp Arg Ile Met Glu Arg
                    95                     100                     105

Gly Ser Tyr Thr Glu Lys Asp Ala Ser His Leu Val Gly Gln Val
                   110                     115                     120

Leu Gly Ala Val Ser Tyr Leu His Ser Leu Gly Ile Val His Arg
                   125                     130                     135

Asp Leu Lys Pro Glu Asn Leu Leu Tyr Ala Thr Pro Phe Glu Asp
                   140                     145                     150

Ser Lys Ile Met Val Ser Asp Phe Gly Leu Ser Lys Ile Gln Ala
                   155                     160                     165

Gly Asn Met Leu Gly Thr Ala Cys Gly Thr Pro Gly Tyr Val Ala
                   170                     175                     180

Pro Glu Leu Leu Glu Gln Lys Pro Tyr Gly Lys Ala Val Asp Val
                   185                     190                     195

Trp Ala Leu Gly Val Ile Ser Tyr Ile Leu Leu Cys Gly Tyr Pro
                   200                     205                     210

Pro Phe Tyr Asp Glu Ser Asp Pro Glu Leu Phe Ser Gln Ile Leu
                   215                     220                     225

Arg Ala Ser Tyr Glu Phe Asp Xaa Pro Phe Trp Asp Asp Ile Ser
                   230                     235                     240

Glu Ser Gly Lys Asp Phe Ile Arg His Leu Leu Glu Arg Asp Leu
                   245                     250                     255

Gln Lys Arg Phe Thr Cys Gln Gln Ala Leu Arg Asp Leu Trp Ile
                   260                     265                     270

Phe Trp Asp Thr Gly Phe Gly Arg Asp Ile Leu Gly Phe Val Ser
                   275                     280                     285

Glu Gln Ile Arg Lys Asn Phe Ala Trp Thr His Trp Lys Arg Ala
                   290                     295                     300

Phe Asn Ala Thr Leu Phe Leu Arg His Ile Arg Lys Leu Gly Gln
                   305                     310                     315

Ile Pro Glu Gly Glu Gly Ala Ser Glu Gln Gly Met Xaa Arg His
                   320                     325                     330
```

10

Ser His Xaa Gly Leu Arg Ala Gly Gln Pro Pro Lys Trp
                    335   340

<210> 7
<211> 20
<212> DNA
<213> Artificial sequence

<220>
<223> Task 110 Forward primer

<400> 7
 agaagtgtgc cagcttcaaa 20

<210> 8
<211> 28
<212> DNA
<213> Artificial sequence

<220>
<223> Task 110 Reverse primer

<400> 8
 ctagatagga tgtcttccac taatcttt 28

<210> 9
<211> 20
<212> DNA
<213> Artificial sequence

<220>
<223> Task 110 Probe

<400> 9
 ccaggcatcg cccttaagcc 20

<210> 10
<211> 20
<212> DNA
<213> Artificial sequence

<220>
<223> Task 119 Forward primer

<400> 10
 tgccaacagt ggattgagtt 20

<210> 11
<211> 20
<212> DNA
<213> Artificial sequence

<220>
<223> Task 119 Reverse Primer

<400> 11
 tgaaggtttg gctcagttca 20

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<210> 12
<211> 24
<212> DNA
<213> Artificial sequence

<220>
<223> Task 119 Probe

<400> 12
 tagctccaag ccttctcctg cctc 24

<210> 13
<211> 512
<212> DNA
<213> Artificial sequence

<220>
<223> Task 110 probe

<400> 13
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 gaaactccaa ttaaaatacc agtaaattca acaggaacag acaagttaat 100

 gacaggtgtc attagccctg agaggcggtg ccgctcagtg gaattggatc 150

 tcaaccaagc acatatggag gagactccaa aaagaaaggg agccaaagtg 200

 tttgggagcc ttgaaagggg gttggataag gttatcactg tgctcaccag 250

 gagcaaaagg aagggttctg ccagagacgg gcccagaaga ctaaagcttc 300

 actataatgt gactacaact agattagtga atccagatca actgttgaat 350

 gaaataatgt ctattcttcc aaagaagcat gttgactttg tacaaaaggg 400

 ttatacactg aagtgtcaaa cacagtcaga ttttgggaaa gtgacaatgc 450

 aatttgaatt agaagtgtgc cagcttcaaa aacccgatgt ggtgggtatc 500

 aggaggcagc gg 512

<210> 14
<211> 584
<212> DNA
<213> Artificial sequence

<220>
<223> Task 119 probe

<400> 14
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 aggctgccgt gctcttccgc cagatggcca ccgccctggc gcactgtcac 100

 cagcacggtc tggtcctgcg tgatctcaag ctgtgtcgct ttgtcttcgc 150

 tgaccgtgag aggaagaagc tggtgctgga gaacctggag gactcctgcg 200
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```
tgctgactgg gccagatgat tccctgtggg acaagcacgc gtgcccagcc 250

tacgtgggac ctgagatact cagctcacgg gcctcatact cgggcaaggc 300

agccgatgtc tggagcctgg gcgtggcgct cttcaccatg ctggccggcc 350

actacccctt ccaggactcg gagcctgtcc tgctcttcgg caagatccgc 400

cgcggggcct acgccttgcc tgcaggcctc tcggcccctg cccgctgtct 450

ggttcgctgc ctccttcgtc gggagccagc tgaacggctc acagccacag 500

gcatcctcct gcacccctgg ctgcgacagg acccgatgcc cttagctcca 550

acccgattcc ctttagtgag ggttaatttc atag 584
```

<210> 15
<211> 641
<212> DNA
<213> Artificial sequence

<220>
<223> Task 120 probe

<400> 15
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gggtggcgag ctgtttgacc gcatcatgga gcgcggctcc tacacagaga 50

aggatgccag ccatctggtg ggtcaggtcc ttggcgccgt ctcctacctg 100

cacagcctgg ggatcgtgca ccgggacctc aagcccgaaa acctcctgta 150

tgccacgccc tttgaggact cgaagatcat ggtctctgac tttggactct 200

ccaaaatcca ggctgggaac atgctaggca ccgcctgtgg gacccctgga 250

tatgtggccc cagagctctt ggagcagaaa ccctacggga aggccgtaga 300

tgtgtgggcc ctgggcgtca tctcctacat cctgctgtgt gggtaccccc 350

ccttctacga cgagagcgac cctgagctct tcagccagat cctgagggcc 400

agctatgagt ttgactctcc tttctgggat gacatctcag aatcagccaa 450

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gccaacaggc cttgcggcac ctttggatct ctggggacac agccttcgac 550

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